We Claim:

1. A vascular endothelial growth factor receptor (VEGFR) comprising a ligand binding pocket that is defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or in a related set of structural coordinates having a root mean square deviation of not more than about 0.90 Å away from the binding pocket Cα atoms of the ligand binding pocket defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

2. The VEGFR according to claim 1, wherein the VEGFR is VEGFR2 kinase domain of SEQ ID NO: 3, or a conservatively substituted variant thereof.

3. An isolated peptide consisting of a ligand binding pocket that is defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or in a related set of structural coordinates having a root mean square deviation of not more than about 0.90 Å away from the binding pocket Cα atoms of the ligand binding pocket defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

4. A vascular endothelial growth factor receptor (VEGFR) comprising a ligand binding pocket that is of approximate dimensions 12 Å x 9 Å x 25 Å.

5. A vascular endothelial growth factor receptor (VEGFR) comprising a ligand binding pocket as depicted in Figure 1, Figure 2A, or Figure 2B.

6. An isolated peptide consisting of a ligand binding pocket as depicted in Figure 1, Figure 2A, or Figure 2B.

7. A vascular endothelial growth factor receptor (VEGFR) comprising a ligand binding pocket that is defined by the structural coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2 or a conservatively substituted variant thereof.

8. A vascular endothelial growth factor receptor (VEGFR) comprising an activation loop defined by amino acid residues 1046 to 1075 of SEQ ID NO: 2, or a conservatively substituted variant thereof, as depicted in Figure 1.

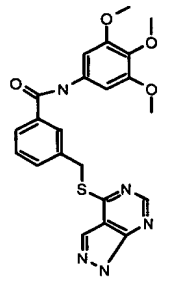
9. An isolated peptide consisting of a ligand binding pocket that is defined by the structural coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2 or a conservatively substituted variant thereof.

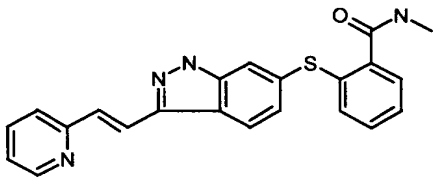
10. An isolated peptide consisting of an activation loop defined by amino acid residues 1046 to 1075 of SEQ ID NO: 2, or a conservatively substituted variant thereof, as depicted in Figure 1.

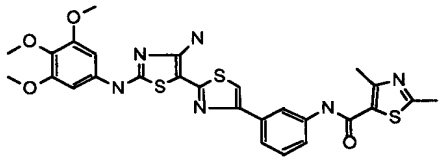
11. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR) peptide: ligand complex, wherein the crystalline structure is defined by the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of structural coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

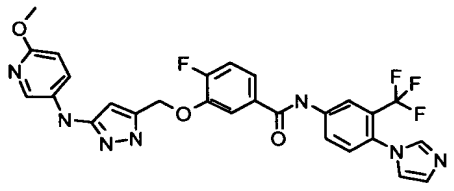
12. The crystalline structure according to claim 11, wherein the VEGFR is VEGFR2 kinase domain of SEQ ID NO: 3, or a conservatively substituted variant thereof.

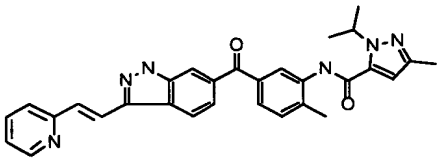
13. The crystalline structure according to claim 11, wherein the ligand is selected from the group consisting of:


;


;


;


;


;

and mixtures thereof.

14. A crystalline structure of an isolated peptide: ligand complex, wherein the crystalline structure is defined by the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of structural coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

15. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR) comprising a ligand binding pocket that is defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or in a related set of structural coordinates having a root mean square deviation of not more than about 0.90 Å away from the binding pocket Cα atoms of the ligand binding pocket defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

16. The crystalline structure according to claim 15, wherein the VEGFR is VEGFR2 kinase domain of SEQ ID NO: 3, or a conservatively substituted variant thereof.

17. A crystalline structure of an isolated peptide: ligand complex, wherein the peptide consists of a ligand binding pocket that is defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or in a related set of structural coordinates having a root mean square

deviation of not more than about 0.90 Å away from the binding pocket Cα atoms of the ligand binding pocket defined by the atoms found in the structural coordinates set forth in Tables 1, 2, 3, 4 or 5.

18. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR): ligand complex, wherein the VEGFR comprises a ligand binding pocket that is of approximate dimensions 12 Å x 9 Å x 25 Å.

19. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR): ligand complex, wherein the VEGFR comprises a ligand binding pocket as depicted in Figure 1, Figure 2A, or Figure 2B.

20. A crystalline structure of an isolated peptide: ligand complex, wherein the peptide consists of a ligand binding pocket as depicted in Figure 1, Figure 2A, or Figure 2B.

21. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR): ligand complex, wherein the VEGFR comprises a ligand binding pocket that is defined by the structural coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2 or a conservatively substituted variant thereof.

22. A crystalline structure of a vascular endothelial growth factor receptor (VEGFR): ligand complex, wherein the VEGFR comprises an activation loop defined by amino acid residues 1046 to 1075 of SEQ ID NO: 2, or a conservatively substituted variant thereof, as depicted in Figure 1.

23. A crystalline structure of an isolated peptide: ligand complex, wherein the peptide consists of a ligand binding pocket that is defined by the structural coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2 or a conservatively substituted variant thereof.

24. A crystalline structure of an isolated peptide: ligand complex, wherein the peptide consists of an activation loop defined by amino acid residues 1046 to 1075 of SEQ ID NO: 2, or a conservatively substituted variant thereof, as depicted in Figure 1.

25. Three-dimensional structural coordinates of a peptide: ligand complex, comprising:

a vascular endothelial growth factor receptor (VEGFR), or a peptide that is structurally related thereto; and

a ligand,

wherein the complex has the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of structural coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the structural coordinates as set forth in Tables 1, 2, 3, 4 or 5.

26. A method of utilizing molecular replacement to obtain structural information about a crystalline molecule or a crystalline molecular complex of unknown structure comprising:

generating an X-ray diffraction pattern from said crystallized molecule or molecular complex; and

applying at least a portion of the structural coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of structural coordinates having a root mean square deviation of not more than about 1.25

Å away from the core Cα atoms of the structural coordinates as set forth in Tables 1, 2, 3, 4 or 5, to the X-ray diffraction pattern to generate a three-dimensional electron density map of at least a portion of the molecule or molecular complex whose structure is unknown.

27. A machine-readable medium having stored thereon data comprising the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5, or a related set of structural coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the structural coordinates as set forth in Tables 1, 2, 3, 4 or 5.

28. A method for generating a three-dimensional computer representation of a molecule comprising a vascular endothelial growth factor receptor kinase domain (VEGFRKD), or a peptide that is structurally related thereto, comprising applying the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5, to a computer algorithm to generate a three-dimensional representation of the molecule.

29. A method for generating a three-dimensional computer representation of a vascular endothelial growth factor receptor (VEGFRKD) ligand binding pocket or VEGFRKD-like ligand binding pocket comprising applying the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 0.90 Å away from the core Cα atoms of the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5, to a computer algorithm to generate a three-dimensional representation of the binding pocket.

30. The method according to claim 29, wherein the ligand binding pocket is defined by the structural coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.

31. A method of using a three-dimensional vascular endothelial growth factor receptor (VEGFR) kinase domain: ligand crystalline structure to identify a potential VEGFR modulator, comprising:

(a) selecting a potential modulator by performing rational drug design using a three-dimensional structure defined by at least a portion of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 1.25 Å away from the core Cα atoms of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5;

(b) contacting the potential modulator with a VEGFR polypeptide; and

(c) detecting whether the potential modulator binds with the polypeptide.

32. The method according to claim 31, wherein , wherein the selection is performed in conjunction with computer modeling.

32. The method according to claim 31, wherein the three-dimensional structure comprises a ligand binding pocket defined by the atomic coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.

33. A method for evaluating the potential of a chemical entity to associate with a vascular endothelial growth factor receptor kinase domain (VEGFRKD) ligand binding pocket or VEGFRKD-like ligand binding pocket comprising:

(a) employing computational means to perform a fitting operation between the chemical entity and a ligand binding pocket defined by at least a portion of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 0.90 Å away from the core Cα atoms of the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5; and

(b) analyzing the results of the fitting operation to quantify the association between the chemical entity and the binding pocket.

34. The method according to claim 33, wherein the ligand binding pocket is defined by the atomic coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.

35. A method for evaluating the ability of a chemical entity to associate with a molecule or molecular complex comprising a vascular endothelial growth factor receptor kinase domain (VEGFRKD) ligand binding pocket or VEGFRKD-like ligand binding pocket, comprising

(a) constructing a computer model of a ligand binding pocket defined by at least a portion of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 0.90 Å away from the core Cα atoms of the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5;

(b) selecting a compound to be evaluated by a method selected from the group consisting of: (i) assembling molecular fragments into a compound, (ii) selecting a compound from a small molecule database, (iii) *de novo* ligand design of a compound, and (iv) modifying a known modulator, or a portion thereof, of a VEGFR;

(c) employing computational means to perform a fitting program operation between a computer model of the compound to be evaluated and the computer model of the ligand binding pocket to provide an energy-minimized configuration of the compound in the binding pocket; and

(d) evaluating the results of the fitting operation to quantify the association between the compound and the binding pocket model.

36. The method according to claim 35, wherein the ligand binding pocket is defined by the atomic coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.

37. A method for identifying a modulator of a molecule comprising a vascular endothelial growth factor receptor kinase domain (VEGFRKD) ligand binding pocket or VEGRKD-like ligand binding pocket, comprising:

(a) generating a three-dimensional structure of the VEGFRKD or VEGFRKD-like ligand binding pocket by applying at least a portion of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 0.90 Å away from the core Cα atoms of the atomic coordinates as set forth in Tables 1, 2, 3, 4 or 5, to a computer algorithm to generate a three-dimensional structural representation of the binding pocket;

(b) employing the three-dimensional structure to design or select the modulator;

(c) synthesizing or obtaining the modulator; and

(d) contacting the modulator with the molecule to determine the ability of the modulator to interact with the molecule.

38. The method according to claim 37, wherein the ligand binding pocket is defined by the atomic coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.

39. A method for identifying a modulator of a molecule comprising a vascular endothelial growth factor receptor kinase domain (VEGFRKD) ligand binding pocket or VEGFRKD-like ligand binding pocket, comprising:

(a) constructing a computer model of the binding pocket;

(b) selecting a compound to be evaluated as a modulator by a method selected from the group consisting of: (i) assembling molecular fragments into a compound, (ii) selecting a compound from a small molecule database, (iii) *de novo* ligand design of a compound, and (iv) modifying a known inhibitor, or a portion thereof, of a VEGFR polypeptide;

(c) employing computational means to perform a fitting program operation between computer models of the compound to be evaluated and the binding pocket in order to provide an energy-minimized configuration of the compound in the binding pocket;

(d) evaluating the results of the fitting operation to quantity the association between the compound and the binding pocket model;

(e) synthesizing the compound; and

(f) contacting the compound with the molecule to determine the ability of the compound to modulate the kinase activity of the molecule,

wherein the ligand binding pocket is defined by at least a portion of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5, or a related set of atomic coordinates having a root mean square deviation of not more than about 0.90 Å away from the core Cα atoms of the atomic coordinates set forth in Tables 1, 2, 3, 4 or 5.

40. The method according to claim 41, wherein the ligand binding pocket is defined by the atomic coordinates of the following amino acid residues: L840, V848, E850, A866, V867, K868, E885, I888, L889, I892, V898, V899, V914, V916, E917, F918, K920, F921, N923, L1019, C1024, I1025, H1026, L1035, I1044, C1045, D1046, and F1047 of SEQ ID NO: 2, or a conservatively substituted variant thereof.